

SEQUENCE LISTING

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<120> Escape Mutants of Newcastle Disease Virus as Marker Vaccines

<130> AM100044

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<170> PatentIn version 3.2

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<212> DNA
<213> Paramyxovirus/Newcastle Disease Virus

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Val Arg Val Ala Leu Ala Leu Ser Cys Val Cys Pro Thr Ser Ser Leu	
20 25 30	
gat ggc agg cct ctt gca gct gca ggg att gtg gtg aca gga gac aaa	144
Asp Gly Arg Pro Leu Ala Ala Ala Gly Ile Val Val Thr Gly Asp Lys	
35 40 45	
gca gtc aac ata tac acc tca tct cag aca ggg tca atc ata gtc aag	192
Ala Val Asn Ile Tyr Thr Ser Ser Gln Thr Gly Ser Ile Ile Val Lys	
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Leu Leu Pro Asn Met Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro	
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ttg gag gcg tac aac agg aca ttg act act ttg ctc acc ccc ctt ggt	288
Leu Glu Ala Tyr Asn Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly	
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Asp Ser Ile Arg Arg Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Gly	
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aaa cag gga cgc ctt ata ggc gcc att atc ggc ggt gca gct ctc ggg	384
Lys Gln Gly Arg Leu Ile Gly Ala Ile Ile Gly Gly Ala Ala Leu Gly	
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gtt gca acc gct gca cag ata aca gca gct tcg gct ctg ata caa gcc Val Ala Thr Ala Ala Gln Ile Thr Ala Ala Ser Ala Leu Ile Gln Ala 130 135 140	432
aac caa aat gct gcc aac atc ctc cgg ctt aaa gag aga att gct gca Asn Gln Asn Ala Ala Asn Ile Leu Arg Leu Lys Glu Arg Ile Ala Ala 145 150 155 160	480
acc aat gag gct gtg cac gag gtc act gat gga tta tca caa cta gca Thr Asn Glu Ala Val His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala 165 170 175	528
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cta gct ggt ggg aat atg gat tac ttg ttg act aag tta ggt gta ggg Leu Ala Gly Gly Asn Met Asp Tyr Leu Leu Thr Lys Leu Gly Val Gly 245 250 255	768
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cct att ctg tac gac tca cag act cag ctc ttg ggt ata cag gta acc Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr 275 280 285	864
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tct cta ata gat agg caa tca tgc aat gtc cta tcc tta gac gga ata Ser Leu Ile Asp Arg Gln Ser Cys Asn Val Leu Ser Leu Asp Gly Ile 420 425 430			1296
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Pro Ile Leu Tyr Asp Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr
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Leu Pro Ser Val Gly Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu
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Thr Leu Ser Val Ser Thr Thr Lys Gly Phe Ala Ser Ala Leu Val Pro
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Lys Val Val Met Lys Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser
 325 330 335

Tyr Cys Ile Glu Thr Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr
 340 345 350

Phe Pro Met Ser Pro Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser
 355 360 365

Ala Cys Met Tyr Ser Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met
 370 375 380

Thr Leu Lys Gly Ser Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg
 385 390 395 400

Cys Ala Asp Pro Pro Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val
 405 410 415

Ser Leu Ile Asp Arg Gln Ser Cys Asn Val Leu Ser Leu Asp Gly Ile
 420 425 430

Thr Leu Arg Leu Ser Gly Glu Phe Asp Ala Thr Tyr Gln Lys Asn Ile
 435 440 445

Ser Ile Gln Asp Ser Gln Val Ile Val Thr Gly Asn Leu Asp Ile Ser
 450 455 460

Thr Glu Leu Gly Asn Val Asn Asn Ser Ile Ser Asn Ala Leu Asp Lys
465 470 475 480

Leu Glu Glu Ser Asn Ser Lys Leu Asp Lys Val Asn Val Lys Leu Thr
485 490 495

Ser Thr Ser Ala Leu Ile Thr Tyr Ile Val Leu Thr Val Ile Ser Leu
500 505 510

Val Cys Gly Ile Leu Ser Leu Val Leu Ala Cys Tyr Leu Met Tyr Lys
515 520 525

Gln Lys Ala Gln Gln Lys Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu
530 535 540

Asp Gln Met Arg Ala Thr Thr Lys Met
545 550